





Figure 5

Sample ID (comment); R4A3F37m1957

Dalabase searched: NCBInr. 7.5.97 Molecular weight search (1000 - 100000 Da) selects 269572 entries. Species search (HOMO SAPIENS) selects 22771 entries.

Combined molecular weight and species scarches select 20933 entries. Number of sequences passing through parent mass filter. 84015 Ion Types Considered: a b B y n h I

search selects 257 entries.

Search

unmodified Hydrogen (II) Free Acid (O II) Peptide C terminus Peptide Masses Digest Max. # Missed Cysteines Peptide is are Used Cleavages Modified by N terminus Par(mi)Frag(av) No enzyme I unmodified Hydrogen (II) Search Made Unnatched Ions are Search Search Par(mi)Frag(av) No enzyme Parent mass: 1957.2000 (+/- 500.0000 ppm)

Fragment Ions used in search: 175.5, 230.3, 331.5, 387.1, 414.1, 431.7, 442.7, 448.8, 460.8, 533.8, 605.0, 704.2, 1224.8, 1425.5, 1628.6, 1801.4, 1914.9, 1940.8 (+/- 2500.00 ppm)
Composition Ions present: [RPJV[NR]][KQ]FSDR

Result Summary

# Unmatched Protein Name Ions	2 (D82930) III.A-A26 variant	2 (U25971) MHC class Lantigen 1II.A-A2407	2 (X82161) III.A.A alpha1 and alpha2 domains	2 (D32129) III.A-A26	2 (Z97370) hunnan leukocyte antigen	2 (U18930) MHC class I antigen HLA-A2	2 (M16010) III.A-A11 class I antigen (AA at 30)	2 (AF017310) MHC class I antigen	2 (A1017309) MHC class I antigen :	2 (AF012767) MHC class Lantigen HLA-A heavy chain
Umn										
Sequence	(Y) <u>VDDTQFVRFDSDAASQR</u> (M)	(Y)VDDTQFVRFDSDAASQR(M)	(Y)VDDTQFVRFDSDAASQR(M)	(Y)VDDTQFVRFDSDAASQR(M)	(Y)VDDTQFVRFDSDAASQR(M)	(Y) <u>VDDTQFVRFDSDAASQR</u> (M)	(Y)VDDTQFVRFDSDAASQR(M)	(Y) <u>VDDTQFVRFDSDAASQR</u> (M)	(Y)VDDTQFVRFDSDAASQR(M)	(Y) <u>VDDTQFVRFDSDAASQR</u> (M)
Calculated Brror MH+ (Da) (Da)	21251.4 HOMO 1956.9052 0.2948 SAPIENS	40679.8 HOMO 1956.9052 0.2948 SAPIENS	20921.2 110MO 1956.9052 0.2948 SAPIENS	41113.1 HOMO 1956.9052 0.2948	38703.4 HOMO 1956.9052 0.2948 SAPIENS	40895.1 HOMO 1956.9052 0.2948 SAPIENS	38355.8 SAPIENS 1956.9052 0.2948	10423.4 HOMO 1956.9052 0.2948 SAPIENS	10430.3 HOMO 1956.9052 0.2948	21027.3 HOMO 1956.9052 0.2948 SAPIENS 1956.9052 0.2948
Species	OMO	OMO	OMO	OMO	OMO	OMO	OMO	OMO	OMO	OMO
7 Protein MW S (Da)	21251.4 ^H /S/	40679.8 ¹¹ 8.8	20921.2 ¹¹ !	41113.1 ^{El}	38703.4 ¹¹⁰	40895.1 ¹¹⁽ S/	38355.8 ¹¹⁽	10423.4 ¹¹⁰	10430.3 ^{LK}	21027.3 ^{HC} SA
Rank MS-DigestNCBInr.7.5.97 Protein index# Accession# (Da)	1839795	915219	825673	994765	2505934	717123	785055	2394324	2394322	2394009
MS-Digestl index#	240839	152874	141923	159176	282322	133479	49436	277806	277805	277713
Rank	1	- 1	1		-1	-1	-1	-1	-1	-1

Figure 5 <u>qb|H23377|H23377</u> ym57e02.rl Homo saplena cOHA clene 52227 5' similar to db:X00492 cds1 HLA CLASS 1 H:STOCOMPATIBILITY ANTIGEM, A-3 A-0301 Lanjeh - 439 9DIANS486561AAS48626 3) 19402.31 HCL_CRAP_ANT HOMO SAPIMAS SCHIM CLORE HW. Eli-19-155 Similar to 90:216633 HLA CLASS 1 HISTOCORPATIOLICITY ANTICIONAL A-2 A-0-00: ALPHA (HURBH); Langth + 539 <u>abirijooffrijoof</u> yf62c03.rl Ress yspiens oom clone 26701 5' similer to apsigevite addi HLA CLASS I BISTOCOMPATIBILITY ANTIGEN, A-23(A-3) Lesth - 159 Lesth - 159 <u>qpinal471511Aaj47151</u> 2032006.r; Stratagene colon (1937201) Roos sapiens cibil did cibil S8591 f' similar to pord6470 RiA CIASS ! RISTOCHMARIDILITY ARTIGEN, A-241A-91 A-2402 ALPIN (RUZUL); Length = 581 Score - 30 (41.7 bits), Expans - 6.1c-05, F - 9.1c-05 Identities - 17/18 (100:), Positives - 19/18 (100:), Frame - -2 Score - 90 (41.9 bits), Expect - 8.1e-05, P - 8.1e-05 Identities - 19718 (1001), Fositives - 18718 (1001), Frame - -1 Score - 90 (41.9 bits), Expert - 8.1m-65, P - 8.1m-61 Identitins - 18/10 11001), Positions - 18/19 (1204), Frame - +1 Score - 70 (41.9 bita), Expec: - 8.10-75, P - 0.1n-05 Identities - 11/18 [1004], Postitives - 18/18 (1001), Frame - +2 Query: I VDDTAFVREDSDAAGORI 19 VDDTQFYREDSDAAGORI Sbjær: 152 VEDTQFVREDSDAASGAI 205 Ouery: | VCDTOFVRFDSDAASCR: 18 VCDTOFVRFDSDAASORH Sbjet: 154 VCDTOFVRFDSDAASORH 207 Ouery: | VEDIOFYREDSDAASOPH 18 VEDIOFYREDSDAAASOPH SDJCt: | 116 VEDIOFYREDSDAAASOPH 1999 L VENTGEVRENSDAASORII 18 VOSTOEVRENSDAASORII 13 VONTGEVRENSDAASORII 66 Plus Strand HSFs: Plus Strand HSPs: Plus Strand MSPs: Plus Strand HSFa: Sbjct: Query: <u>obinizodé prisidio el Homo sapiens como cione 26062 5' similar en 190700472 casi Hua Class I Histocomparibility anticen, a-3 a-0301 lenten - 405</u> <u>qbinspretingstre</u> yhd?cob.rt Homa sapiens cikin cione 42563 5' stailar to pp:700492 cast HLA CLASS 1 HISTOCKHPATIBILITY AHTIGEB, A-3 A-0301 APRA (HPSAH). <u>401A44885341A4488114</u> +D37109.rl Stratagene Hela cell s3 97216 Homo s472-Ans 2014 Clone 843015 5' similar to poi.05615 Hla CLASS 1 Hla Cl QDIAN1226331An123653 ro21a05.r1 Stratages colon (1937704) Homo suptens colon (2037704) HLA CLASS thilar to abiz1665) HLA CLASS this ros abiz1665) HLA CLASS this colon content interference in the class of his colon and the class this colon and the class this colon and the class this colon and the class of the class this colon and the class this Score + 90 (41.7 bits), Espect - 9.1e-05, P = 9.1e-05 Identities + 13/19 (1901), Positives + 18/18 (1901), Frame - +2 Score = 90 (41.9 bits), Expact = 3.1e-05, P = 9.1e-05 Identities = 13/18 (1001), Positives = 19/18 (1001), Frame = +3 Score - 70 [41.9 bits], Expect - 8.14-55, P - 6.16-35 Identities - 13/18 (1001), Positives - 13/18 (1001), Frame - +1 Score - 90 (41.9 bits), Espect - 4.1e-75, P - 8.1e-75 Identities - 18/18 (1001), fosttives - 18/18 (1001), Frame - 13 Outry: I VOCTOFYRESSOAASOR! 18 VCDTOFVRESSOAASOR! SDjet: 154 VCDTOFYRFOSDAASOR! 211 Query: 1 VDDTOF/RFDSDANSQRH 18 VDDTOFVRFDSDANSQRH Sbjet: 150 VDDTOFVRFDSDANSQRH 203 Query: 1 VCDTOFVREDSDAASORH 18 VCDTOFVREDSCAASORH Sbjet: 157 VDDTOFVREDSDAASQRH 210 Ouery: 1 VODTOFTPEDSDAASOR: 19 VODTOFTPETSSCAASOR: Sbjct: 138 VODTOFVRFDSDAASORH 191 Plus Strand RSFs: Plus Strand HSPs: Plus Strand HSPs: Plus Strand 45Ps:

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